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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
SWOPE, SHERIDAN	
ART UNIT	**PAPER NUMBER**
1652	14

DATE MAILED: 07/25/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/008,355	TRAVIS ET AL.	
	Examiner	Art Unit	
	Sheridan L. Swope	1652	

-- The MAILING DATE of this communication appears on the cov r sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *15 May 2003* .

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *39-53* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *39-53* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11)☐ The proposed drawing correction filed on _____ is: a)☐ approved b)☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12)☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____ .

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

14)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. § 119(e) (to a provisional application).

a) ☐ The translation of the foreign language provisional application has been received.

15)☐ Acknowledgment is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s) *12* .
4) ☐ Interview Summary (PTO-413) Paper No(s). _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: .

DETAILED ACTION

Applicant's response, on May 15, 2003, Paper No. 13, to the first Office Action on the Merits of this case is acknowledged. It is acknowledged that applicants have cancelled Claims 10-18 and 24-38 and added Claims 29-53. Claims 29-53 are hereby considered.

Claim Rejections - 35 USC § 112-Second Paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

In Paper No. 11, Claims 10-12 and 24-38 were rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Said rejection is withdrawn because Claims 10-12 and 24-38 have been cancelled. However, new Claims 39, 41-53 are hereby rejected for the same reason described in the prior action. Applicants argue that: (i) the specification states that "aliphatic residue" means an organic radical having carbon atoms linked in open chains, and that "aromatic residue" means an organic radical that includes an aromatic ring; (ii) it would be clear to one of skill in the art that glycine has neither an aliphatic or an aromatic residue and that tyrosine has an aliphatic or aromatic residue. Applicants request clarification of the Examiner's question asking if tyrosine is considered to be "polar or aromatic".

Said arguments are not found to be persuasive. Based on the definitions above, it is unclear whether "aliphatic residue" includes alanine, valine, leucine, isoleucine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, methionine, lysine, and/or arginine and whether "aromatic residue" includes phenylalanine, tyrosine, and/or tryptophan. The Examiner's original question asking whether tyrosine is considered to be polar or aromatic can be rephrased

as: Do the applicant's consider tyrosine to be an aromatic residue in light of tyrosine's polar nature? Applicant's statement in Paper No. 13 that tyrosine has an aliphatic or aromatic residue points out the indefiniteness of Claims 39, 41-53, as tyrosine is not comprised of "carbon atoms linked in open chains", which is the definition of "aliphatic residue" on page 6 of the specification. Thus without reciting specific amino acid residues, Claims 39, 41, 44, and 50, as well as Claims 42, 43, 45-49, and 51-53, which are dependent thereon, are indefinite. Therefore, Claims 39 and 41-53 are rejected under 35 U.S.C. 112, second paragraph, for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 39 and 41-53 rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. In Claim 39, recitation of the phrase "... active modification of the peptidase..." on lines 6 and 7 renders the claim indefinite, as modification is not a noun. Claims 41`-53, which are dependent from Claim 39, are indefinite for the same reason. For purposes of examination, it is assumed that said phrase is meant to recite "...active variant of the peptidase...". Correction is required.

Claims 44-49 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. On lines 10-11 of Claim 44, recitation of a catalytic domain having a percentage amino acid identity of greater that 40% with SEQ ID NO: 2 renders Claim 44 indefinite. It is not clear what specific residues of SEQ ID NO: 2, or any other recited dipeptidases, comprise the catalytic domain. It is also not clear whether Claim 44 is meant to recite any polypeptide

wherein the catalytic domain has greater than 40% identity with the catalytic domain of SEQ ID NO: 2 or greater than 40% identity with the full-length of SEQ ID NO: 2. Claims 45-49 are rejected for the same reasons. For purposes of examination, it is assumed that the catalytic domain of SEQ ID NO: 2 consists of residues 522-712 and that Claim 44 is meant to recite any polypeptide wherein the catalytic domain has greater than 40% identity with the catalytic domain of SEQ ID NO: 2.

Claim Rejections - 35 USC § 112-First Paragraph

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

In Paper No. 11, Claims 10, 12, 13, and 24-31 were rejected under 35 U.S.C. 112, first paragraph. Said rejection is withdrawn because Claims 10, 12, 13, and 24-31 have been cancelled. However, new Claims 39, 41-50 are hereby rejected for the same reason described in the prior action. Applicants argue that the specification provides guidance on how to make the claimed nucleic acid molecules and that the specification includes working examples of the claimed isolated nucleic acids. Applicants further state that (i) the nucleic acid molecules of Claim 39 have been sufficiently described based on the recitation of "at least 20 nucleotides hybridize to SEQ ID NO: 1" and the recitation of dipeptidase amidolytic activity; (ii) the nucleic acid molecules of Claim 41 have been sufficiently described based on the recitation of a sequence comprising residues 543-712 of SEQ ID NO: 2 and the recitation of dipeptidase amidolytic activity; and (iii) the nucleic acid molecules of Claim 44 have been sufficiently described based on the recitation of a sequence comprising SEQ ID NO: 25 and having greater

than 40% identity with SEQ ID NO: 2 and having dipeptidase amidolytic activity. These arguments are not found to be persuasive. It is acknowledged that the specification teaches the purification of the polypeptide set forth by SEQ ID NO: 2 as well as how to isolate naturally occurring polynucleotides that are homologous to SEQ ID NO: 1 and how to test for amidolytic activity. However, Claims 39, 41-47, and 50 are not limited to naturally occurring polynucleotides encoding proteins with dipeptidase amidolytic activity, but also encompass recombinant variants of SEQ ID NO: 2. Claims 39, 41-47, and 50 are not enabled for the reasons described below.

Although the specification is enabling for the dipeptidypeptidase encoded by SEQ ID NO: 1 and set forth by SEQ ID NO: 2, the specification does not reasonably provide enablement for any nucleic acid molecule encoding any dipeptidylpeptidase amidolytic activity, as recited in Claims 39, 41-47, and 50. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

Claim 39 is so broad as to encompass any nucleic acid molecule encoding any dipeptidylpeptidase activity having amidolytic activity wherein at least about 20 nucleotides hybridize to SEQ ID NO: 1 and wherein the dipeptidylpeptidase amidolytic activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue. Claim 41 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue and wherein said polypeptide comprises residues 543-712 of SEQ ID NO: 2. Claim 42 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase

amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue and wherein said polypeptide comprises residues 540-712 of SEQ ID NO: 2. Claim 43 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue and wherein said polypeptide comprises residues 522-712 of SEQ ID NO: 2. Claim 44 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 40% identity with SEQ ID NO: 2. Claim 45 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 50% identity with SEQ ID NO: 2. Claim 46 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 60% identity with SEQ ID NO: 2. Claim 47 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 70% identity with SEQ ID NO: 2. Claim 50 is so broad as to encompass any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase

amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said nucleic acid molecule has at least 70% identity with SEQ ID NO: 1. The scope of each of these claims is not commensurate with the enablement provided by the disclosure with regard to the extremely large number of polynucleotides broadly encompassed by the claim. Since the amino acid sequence of a protein determines its structural and functional properties, predictability of which changes can be tolerated in a protein's amino acid sequence and obtain the desired dipeptidylpeptidase amidolytic activity requires a knowledge of and guidance with regard to which amino acids in the protein's sequence, if any, are tolerant of modification and which are conserved (i.e. expectedly intolerant to modification), and detailed knowledge of the ways in which the protein's structure relates to its function. However, in this case the disclosure is limited to the amino acid sequence of SEQ ID NO 2 and the nucleotide sequence of SEQ ID NO 1.

While recombinant and mutagenesis techniques are known, it is not routine in the art to screen for multiple substitutions or multiple modifications, as encompassed by the instant claims, and the positions within a protein's sequence where amino acid modifications can be made with a reasonable expectation of success in obtaining the desired activity/utility are limited in any protein and the results of such modifications are unpredictable. In addition, one skilled in the art would expect any tolerance to modification for a given protein to diminish with each further and additional modification, e.g. multiple substitutions.

The specification does not support the broad scope of (i) Claim 39 encompassing any nucleic acid molecule encoding any dipeptidylpeptidase activity having amidolytic activity wherein at least about 20 nucleotides hybridize to SEQ ID NO: 1 and wherein the

dipeptidylpeptidase amidolytic activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue; (ii) Claim 41 any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue and wherein said polypeptide comprises residues 543-712 of SEQ ID NO: 2; (iii) Claim 42 encompassing any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue and wherein said polypeptide comprises residues 540-712 of SEQ ID NO: 2; (iv) Claim 43 encompassing any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue and wherein said polypeptide comprises residues 522-712 of SEQ ID NO: 2; (v) Claim 44 encompassing any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 40% identity with SEQ ID NO: 2; (vi) Claim 45 encompassing any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 50% identity with SEQ ID NO: 2; (vii) Claim 46 encompassing any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 60% identity with SEQ ID

NO: 2; (viii) Claim 47 encompassing any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said polypeptide comprises SEQ ID NO: 25 and the catalytic domain has greater than 70% identity with SEQ ID NO: 2; or (ix) Claims 50 encompassing any nucleic acid molecule encoding a polypeptide having dipeptidylpeptidase amidolytic activity wherein said activity cleaves after a N-terminal penultimate residue which is an aliphatic or aromatic residue and wherein said nucleic acid molecule has at least 70% identity with SEQ ID NO: 1.

The specification does not support the broad scope of Claims 39, 41-47, and 50 because the specification does not establish: (A) regions of the protein's structure which may be modified without effecting the dipeptidylpeptidase amidolytic activity; (B) the general tolerance of the dipeptidylpeptidase amidolytic activity to modification and extent of such tolerance; (C) a rational and predictable scheme for modifying any residues with an expectation of obtaining the desired biological function; and (D) the specification provides insufficient guidance as to which of the essentially infinite possible choices is likely to be successful.

Thus, applicants have not provided sufficient guidance to enable one of ordinary skill in the art to make and use the claimed invention in a manner reasonably correlated with the scope of the claims broadly including any number of nucleic acid molecules encoding proteins with dipeptidylpeptidase activity having an enormous number of amino acid modifications of the dipeptidylpeptidase of SEQ ID NO: 2. The scope of the claims must bear a reasonable correlation with the scope of enablement (In re Fisher, 166 USPQ 19 24 (CCPA 1970)). Without sufficient guidance, determination of the identity of sequences having the desired biological

characteristics is unpredictable and the experimentation left to those skilled in the art is unnecessarily, and improperly, extensive and undue. See In re Wands 858 F.2d 731, 8 USPQ2nd 1400 (Fed. Cir, 1988).

In Paper No. 11, Claims 10, 12, 13, and 24-31 were rejected under 35 U.S.C. 112, first paragraph as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Said rejection is withdrawn because Claims 10-12 and 24-38 have been cancelled. However, new Claims, 39, 41-50, are hereby rejected for the same reasons described in the prior action. Applicants argue that the specification provides guidance in selecting amino acids for substitution within the encoded peptidase (p13, l31 to p14, l10). Applicants also argue that, in view of the present specification, one of skill in the art would be enabled to select appropriate amino acids in the peptidase as candidates for substitution (p14, l11 to p15, l2). It is acknowledged that the specification provides written description for a list of conservative amino acid substitutions for each of hydrophobic, polar, basic, and acidic residues (p 13). The specification also teaches that, preferably, the dipetidylpeptidase includes the sequence TGGNSGSPV or, more preferably, TGGNSGSPVF and that the catalytic domain of the dipetidylpeptidases preferably consist of residues 543-712 of the protein set forth by SEQ ID NO: 2, more preferably consist of residues 540-712 of the protein set forth by SEQ ID NO: 2, or most preferably consist of residues 522-712 of the protein set forth by SEQ ID NO: 2 (p14). However, these arguments are not found to be persuasive.

Claims 39, 41-50 are directed to a genus of DNA molecules encoding any dipeptidylpeptidase amidolytic activity wherein said genus is comprised of a large number of variants of SEQ ID NO: 1 or encode a large number of variants of SEQ ID NO: 2 wherein at least 20 nucleotides of the complement hybridizes to SEQ ID NO: 1 wherein, the catalytic domain comprises residues 543-712, 540-712, or 522-712 of SEQ ID NO: 2, catalytic domain comprises TGGNSGSPVF and has greater than 40%, 50%, 60%, 70%, 80%, or 90% indentity with SEQ ID NO: 2, or polynucleotide has at least 70% identity with SEQ ID NO: 1. The specification teaches the structure of only a single representative species of such DNAs, SEQ ID NO: 1. Moreover, the specification fails to describe any other representative species by any identifying characteristics or properties other than providing a list of conservative amino acid substitutions for each of hydrophobic, polar, basic, and acidic residues (p 13) and teaching that, preferably, the dipetidylpeptidase includes the sequence TGGNSGSPV or, more preferably, TGGNSGSPVF and that the catalytic domain of the dipetidylpeptidases preferably consist of residues 543-712 of the protein set forth by SEQ ID NO: 2, more preferably consist of residues 540-712 of the protein set forth by SEQ ID NO: 2, or most preferably consist of residues 522-712 of the protein set forth by SEQ ID NO: 2. These recited structural features do not constitute a substantial portion of the genus, as the remainder of the structure of any polypeptide with dipeptidylpeptidase amidolytic activity to be encoded by the genus of DNA molecules is completely undefined. Polynucleotides wherein at least 20 nucleotides of the complement hybridizes to SEQ ID NO: 1, wherein the catalytic domain comprises residues 543-712, 540-712, or 522-712 of SEQ ID NO: 2, wherein the catalytic domain comprises TGGNSGSPVF and has greater than 40%, 50%, 60%, 70%, 80%, or 90% indentity with SEQ ID NO: 2, or wherein the

polynucleotide has at least 70% identity with SEQ ID NO: 1 are highly unlikely to encode dipeptidylpeptidase amidolytic activity and the specification does not define the remaining structural features necessary for members of the genus to be selected. Applicants attention is drawn to the distinction between Claims 40 and 51-53 (which have not been rejected) in which the polynucleotides of SEQ ID NO: 1 or having at least 80%, 90%, or 95% identity with SEQ ID NO: 1, are likely to encode polypeptides having dipeptidylpeptidase amidolytic activity, and the rejected claims, 39, 41-50, in which substantial additional undefined sequence is necessary to select a member of the genus. Given this lack of description of representative species encompassed by the genus of the claims, the specification fails to sufficiently describe the claimed invention in such full, clear, concise, and exact terms that a skilled artisan would recognize that applicants were in possession of the claimed invention.

Applicant is referred to the revised guidelines concerning compliance with the written description requirement of U.S.C. 112, first paragraph, published in the Official Gazette and also available at www.uspto.gov.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this

subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

In Paper No. 11, Claims 10-13 and 24-38 were rejected under 35 U.S.C. 102(a) or (b) over applicant's admission of the prior art. Said rejection is withdrawn because Claims 10-13 and 24-38 have been cancelled. However, new Claims 39-53 are hereby rejected for the same reasons described in the prior action. Applicants argue that the independent Claims 39, 41, 44, and 50 recite "an isolated nucleic acid" while the art of the TIGR database disclosing P. Gingivalis genomic contig gln/TIGR/p. gingivalis_1208 discloses contigs that are part of the P. gingivalis genome and that Applicants are not claiming such contigs or the unfinished genome. Applicants also state that Gingivalis genomic contig gln/TIGR/p. gingivalis_1208 provides no guidance as to which sequence of nucleic acids might encode a protein and directs the Examiner's attention to the declaration submitted by Loren Albin on January 7, 2003.

These arguments are not found to be persuasive. Sequencing of the P. Gingivalis genome was performed by preparing a library from P. Gingivalis strain W83 comprised of isolated genomic DNA polynucleotides inserted into either a plamid or phage vector. Isolated vectors comprising the inserted genomic DNA were used for sequencing (Duncan et al, 2002; www.pgingivalis.org/). One or more relevant isolated DNA molecules used for sequencing, including contig gln/TIGR/p. gingivalis_1208, inherently comprise the polynucleotide of SEQ ID NO: 1. Thus, the procedure for sequencing the genome uses isolated polynucleotides from P. Gingivalis comprising SEQ ID NO: 1. The specific polynucleotide sequences encoding dipeptidylpeptidase and amidolytic activities can be easily identified by analyzing the sequence of the P. Gingivalis TIGR database using commercially available programs such as ProSite. As

discussed in the prior action, the specification discloses (Example 6) that contig gln/TIGR/p. gingivalis_1208 from the publicly available data-base TIGR was used to obtain the polynucleotide sequence encoding DPP-7, as presented in Fig 4 and set forth by SEQ ID NO: 2. Disclosure of the sequence for contig gln/TIGR/p. gingivalis_1208 was available to the public in June of 1998 (as per Michael Brown, Paper No. 13, Exhibit B). Therefore, Claims 39, 51-50 are rejected under 35 U.S.C. 102 (b) over applicant's admission of the prior art.

Claims 39 and 41-53 are rejected under 35 U.S.C. 102(e) as being anticipated by Ross et al, 2002 (filing date Dec 23, 1998). Ross et al teach a polynucleotide having 99.8% identity with SEQ ID NO: 1 over 1500 nucleotides (see alignment). Said polynucleotide encodes a polypeptide having 99.6% identity with amino acid residues 137-712 of SEQ ID NO: 2 (see alignment) and having the conserved serine protease motif of SEQ ID NO: 25 (see reading frame 3 from EMBOSS-Transeq). A BLAST search demonstrated that the polypeptide of Ross et al has some homology with known proteases, including a protease comprising the serine protease motif of SEQ ID NO: 25 (see results of BLAST). Thus, a skilled artisan would reasonably believe that the protein of Ross et al inherently has dipeptidylpeptidase amidolytic activity. The Office does not have the facilities to determine whether the sequence taught by Ross et al has dipeptidylpeptidase amidolytic activity. The burden is on the applicant to prove that the polynucleotide taught by Ross et al does not disclose the invention of Claims 39 and 41-53. Therefore, Claims 39-53 are rejected under 35 U.S.C. 102(e) as being anticipate by Ross et al, 2002.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sheridan L. Swope whose telephone number is 703-305-1696. The examiner can normally be reached on M-F; 9:30-7 EST.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapura Achutamurthy can be reached on 703-308-3804. The fax phone numbers for the organization where this application or proceeding is assigned are 703-305-3014 for regular communications and 703-872-9307 for After Final communications.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Sheridan L. Swope, Ph.D.

REBECCA E. PROUTY
PRIMARY EXAMINER
GROUP ~~1800~~
1600